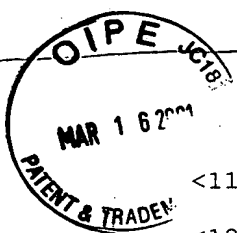


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SEQUENCE LISTING

<110> Bander, Neil H.  
<120> TREATMENT AND DIAGNOSIS OF PROSTATE CANCER  
<130> Lois M. Kwasigroch: BZL 242/026  
<140> US 09/357,709  
<141> 1999-07-20  
<150> US 08/838,682  
<151> 1997-04-09  
<150> US 60/016,976  
<151> 1996-05-06  
<150> US 60/022,125  
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gactgtagac aagtcctcca gtacagccta catggagctc cgcagcctaa catctgagga 300  
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gtaggtggta ccaccattgt taggattgat gtttccaatc cactcaaggc tctttccatg 240  
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10560

B11

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<210> 3  
<211> 123  
<212> PRT  
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<400> 3

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Phe Trp Ile His Ile His Ile Tyr His Thr Leu Gly Glu Ala Glu Pro  
35 40 45  
Trp Lys Glu Pro Val Asp Trp Lys His Gln Ser Gln Trp Trp Tyr His  
50 55 60  
Leu Gln Ser Glu Val Arg Gly Gln Gly His Ile Asp Cys Arg Gln Val  
65 70 75 80  
Leu Gln Tyr Ser Leu His Gly Ala Pro Gln Pro Asn Ile Gly Phe Cys  
85 90 95  
Ser Leu Leu Leu Cys Ser Trp Leu Glu Leu Leu Leu Gly Pro Arg His  
100 105 110  
His Ser His Ser Leu Leu Ser Gln Asn Asp Thr  
115 120

<210> 4  
<211> 130  
<212> PRT  
<213> Mus sp.

<400> 4

Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu Gln Gln  
1 5 10 15  
Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Arg Ile Ser Cys  
20 25 30  
Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His Trp Val Lys  
35 40 45  
Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn  
50 55 60  
Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu  
65 70 75 80  
Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu  
85 90 95

Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe  
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr  
115 120 125

Thr Pro  
130

<210> 5  
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<213> Mus sp.

<400> 5

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Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg  
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Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala  
35 40 45

Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val  
50 55 60

Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser  
65 70 75 80

Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu  
85 90 95

Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys  
100 105 110

Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro  
115 120 125

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<400> 6

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catggaaaga gccttgagtg gattggaaac atcaatccta acaatggtgg taccacctac 180  
aatcagaagt tcgaggacaa ggccacattg actgtagaca agtcctccag tacagcctac 240  
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<212> DNA  
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ggacttgtct acagtcaatg tggccttgct ctcgaacttc tgattgtagg tggtagcacc 180  
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<210> 8  
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<212> PRT  
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<400> 8  
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20 25 30  
Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
35 40 45  
Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe  
50 55 60  
Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr  
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Val Ser Ser  
115

<210> 9  
<211> 363  
<212> DNA  
<213> Mus sp.

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gtaggagaga gggtcacctt gacctgcaag gccagtgaga atgtggttac ttatgtttcc 120  
tggtatcaac agaaaccaga gcagtctcct aaactgctga tatacggggc atccaaccgg 180  
tacactgggg tccccgatcg cttcacaggc agtggatctg caacagattt cactctgacc 240

atcagcagtg tgcaggctga agaccttgca gattatcact gtggacaggg ttacagctat 300  
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<210> 10  
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<212> DNA  
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gatggtcaga gtgaaatctg ttgcagatcc actgcctgtg aagcgatcgg ggacccagct 180  
gtaccgggttg gatgccccgt atatcagcag tttaggagac tgctctgggt tctgttgata 240  
ccaggaaaca taagtaacca cattctcact ggccttgacg gtcaaggtga ccctctctcc 300  
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taa 363

<210> 11  
<211> 121  
<212> PRT  
<213> Mus sp.

<400> 11

Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser  
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Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln  
35 40 45  
Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val  
50 55 60  
Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr  
65 70 75 80  
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln  
85 90 95  
Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile  
100 105 110  
Lys Arg Ala Asp Ala Ala Pro Thr Val  
115 120

<210> 12

<211> 114  
<212> PRT  
<213> Mus sp.

<400> 12

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro  
1 5 10 15

Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu  
20 25 30

Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys  
35 40 45

Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln  
50 55 60

Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu  
65 70 75 80

Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr  
85 90 95

Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln  
100 105 110

Leu Tyr

*BU*  
*BhV*  
<210> 13  
<211> 116  
<212> PRT  
<213> Mus sp.

<400> 13

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His  
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Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu  
20 25 30

Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser  
35 40 45

Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser  
50 55 60

Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln  
65 70 75 80

Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu  
85 90 95

Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys  
100 105 110

Cys Thr Asn Cys  
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 gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180  
 cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240  
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<210> 15  
 <211> 321  
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 agatccactg cctgtgaagc gatcggggac cccagtgtac cggttggatg ccccgatat 180  
 cagcagttta ggagactgct ctggtttctg ttgataccag gaaacataag taaccacatt 240  
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<210> 16  
 <211> 107  
 <212> PRT  
 <213> Mus sp.

<400> 16

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 Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly  
 50 55 60  
 Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala  
 65 70 75 80  
 Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
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<210> 17  
<211> 321  
<212> DNA  
<213> Mus sp.

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ggacaatctc ctaaactact gatttattgg gcatccactc ggcacactgg agtccctgat 180  
cgcttcacag gcagtggatc tgggacagac ttcactctca ccattactaa tgttcagtct 240  
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gggaccatgc tggacctgaa a 321

<210> 18  
<211> 321  
<212> DNA  
<213> Mus sp.

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agatccactg cctgtgaagc gatcagggtac tccagtgtgc cgagtggatg cccaataaat 180  
cagtagttta ggagattgtc ctggtttctg ttgataccag tctacagcag taccacatc 240  
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<210> 19  
<211> 107  
<212> PRT  
<213> Mus sp.

<400> 19

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly  
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Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp Val Gly Thr Ala  
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Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile  
35 40 45  
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser  
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu  
85 90 95

Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys  
100 105

<210> 20  
<211> 125  
<212> PRT  
<213> Mus sp.

<400> 20

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
20 25 30

Tyr Met Asn Asn Trp Val Lys Gln Ser Pro Gly Lys Ser Leu Glu Trp  
35 40 45

Ile Gly Asp Ile Asn Pro Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys  
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala  
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
85 90 95

Cys Ala Arg Gly Tyr Tyr Ser Ser Ser Tyr Met Ala Tyr Tyr Ala Phe  
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
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<210> 21  
<211> 109  
<212> PRT  
<213> Mus sp.

<400> 21

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn  
20 25 30

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu  
35 40 45

Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu

65

70

75

80

BLV  
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro  
85 90 95

Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

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65